

FIG. 1

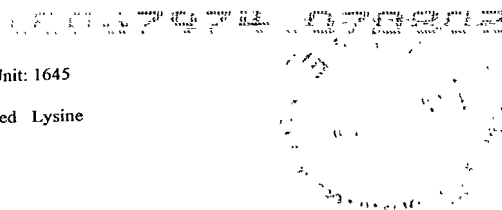
Amino Acid sequence of ATCC 21529 Ask

SEQ ID NO: 1 GTGGCCCTGGTCGTACAGAAATATGGCGGTTCTCGCTTGACAGTGCGGAACGCATTAGA
1 -----+-----+-----+-----+-----+-----+-----+ 60
SEQ ID NO: 2 M A L V V Q K Y G G S S L E S A E R I R
AACGTCGCTGAACGGATCGTTGCCACCAAGAAGGCTCGAAATGATGTCGTGGTTGTCTGC
61 -----+-----+-----+-----+-----+-----+-----+ 120
N V A E R I V A T K K A G N D V V V V C
TCCGCAATGGGAGACACCACGGATGAACCTTCTAGAACTTGCAGCGGCAGTGAATCCCGTT
121 -----+-----+-----+-----+-----+-----+-----+ 180
S A M G D T T D E L L E L A A A V N P V
CCGCCAGCTCGTGAAATGGATATGCTCCTGACTGCTGGTGAGCGTATTTCTAACGCTCTC
181 -----+-----+-----+-----+-----+-----+-----+ 240
P P A R E M D M L L T A G E R I S N A L
GTCGCCATGGCTATTGAGTCCCTTGGCGCAGAAGCTCAATCTTTCACTGGCTCTCAGGCT
241 -----+-----+-----+-----+-----+-----+-----+ 300
V A M A I E S L G A E A Q S F T G S Q A
GGTGTGCTCACCACCGAGCGCCACGGAACGCACGCATTGTTGACGTCACACCGGGTCGT
301 -----+-----+-----+-----+-----+-----+-----+ 360
G V L T T E R H G N A R I V D V T P G R
GTGCGTGAAGCACTCGATGAGGGCAAGATCTGCATTGTTGCTGGTTTTAGGGGTGTTAAT
361 -----+-----+-----+-----+-----+-----+-----+ 420
V R E A L D E G K I C I V A G F Q G V N
AAAGAAACCCGCGATGTCACCACGTTGGGTCGTGGTGGTTCTGACACCACTGCAGTTGCG
421 -----+-----+-----+-----+-----+-----+-----+ 480
K E T R D V T T L G R G G S D T T A V A
TTGGCAGCTGCTTTGAACGCTGATGTGTGTGAGATTTACTCGGACGTTGACGGTGTGTAT
481 -----+-----+-----+-----+-----+-----+-----+ 540
L A A A L N A D V C E I Y S D V D G V Y
ACCGCTGACCCGCGCATCGTTCCTAATGCACAGAAGCTGGAAAAGCTCAGCTTCGAAGAA
541 -----+-----+-----+-----+-----+-----+-----+ 600
T A D P R I V P N A Q K L E K L S F E E
ATGCTGGAACCTTGCTGCTGTTGGCTCCAAGATTTTGGTGCTGCGCAGTGTTGAATACGCT
601 -----+-----+-----+-----+-----+-----+-----+ 660
M L E L A A V G S K I L V L R S V E Y A
CGTGCAATCAATGTGCCACTTCGCGTACGCTCGTCTTATAGTAATGATCCCGGCACTTTG
661 -----+-----+-----+-----+-----+-----+-----+ 720
R A F N V P L R V R S S Y S N D P G T L
ATTGCCGGCTCTATGGAGGATATTCTGTGGAAGAAGCAGTCCTTACCGGTGTGCAACC
721 -----+-----+-----+-----+-----+-----+-----+ 780
I A G S M E D I P V E E A V L T G V A T
GACAAGTCCGAAGCCAAAGTAACCGTTCTGGGTATTTCCGATAAGCCAGGCGAGGCTGCC
781 -----+-----+-----+-----+-----+-----+-----+ 840
D K S E A K V T V L G I S D K P G E A A

FIG.2A

SEQ ID NO: 1
(CONT.) 841 AAGGTTTTCCGTGCGTTGGCTGATGCAGAAATCAACATTGACATGGTTCTGCAGAACGTC 900
-----+-----+-----+-----+-----+-----+
SEQ ID NO: 2 K V F R A L A D A E I N I D M V L Q N V
(CONT.)
901 TCCTCTGTGGAAGACGGCACCACCGACATCACGTTACCTGCCCTCGCGCTGACGGACGC 960
-----+-----+-----+-----+-----+-----+
961 S S V E D G T T D I T F T C P R A D G R
961 CGTGCGATGGAGATCTTGAAGAAGCTTCAGGTTCAAGGCAACTGGACCAATGTGCTTTAC 1020
-----+-----+-----+-----+-----+-----+
1021 R A M E I L K K L Q V Q G N W T N V L Y 1080
1021 GACGACCAGGTCGGCAAAGTCTCCCTCGTGGGTGCTGGCATGAAGTCTCACCCAGGTGTT 1080
-----+-----+-----+-----+-----+-----+
1081 D D Q V G K V S L V G A G M K S H P G V 1140
1081 ACCGCAGAGTTCATGGAAGCTCTGCGCGATGTCAACGTGAACATCGAATTGATTTCCATC 1140
-----+-----+-----+-----+-----+-----+
1141 T A E F M E A L R D V N V N I E L I S I 1200
1141 TCTGAGATCCGCATTTCCGTGCTGATCCGTGAAGATGATCTGGATGCTGCTGCACGTGCA 1200
-----+-----+-----+-----+-----+-----+
1201 S E I R I S V L I R E D D L D A A A R A 1260
1201 TTGCATGAGCAGTTCCAGCTGGGCGGCGAAGACGAAGCCGTCGTTTATGCAGGCACCGGA 1260
-----+-----+-----+-----+-----+-----+
1261 L H E Q F Q L G G E D E A V V Y A G T G
CGCTAA
1261 ----- 1266
R *

FIG.2B



Amino Acid sequence of ATCC 21529 asd

SEQ ID NO: 3 ATGAGCACCATCGCAGTTGTTGGTGCAACCGGCCAGGTCGGCCAGGTTATGCGCAGGTTT
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 SEQ ID NO: 4 M T T I A V V G A T G Q V G Q V M R T F
 TTGGAAGAGCGCAATTTCCCAGCTGAGACTGTTGGTTTCTTTGCTTCCCCCGTTCCGCA
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 L E E R N F P A D T V R F F A S P R S A
 GGCCGTAAGATTGAATTCGTTGGCACGGAATCGAGGTAGAAGACATTACTCAGGCAACC
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 G R K I E F R G T E I E V E D I T Q A T
 GAGGACTCCCTCAAGGGCATCGACGTTGCGTTGTTCTCTGCTGGAGGCACCGCTTCCAAG
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 E E S L K G I D V A L F S A G G T A S K
 CAGTACGCTCCACTGTTTGCTGCTGCAGGCGCGACTGTTGTGGATAACTCTTCTGCTTGG
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 Q Y A P L F A A A G A T V V D N S S A W
 CGCAACGACGACGAGGTTCCACTAATCGTCTCTGAGGTGAACCCCTCCGACAAGGATTCC
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 R K D D E V P L I V S E V N P S D K D S
 CTGGTCAAGGGCATTATTGCGAATCCTAACTGCACCACCATGGCTGCAATGCCAGTGCTG
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 L V K G I I A N P N C T T M A A M P V L
 AAGCCACTGCACGATGCCGCTGGTCTTGTAAGCTTCACGTTTCCTCTTACCAGGCTGTT
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 K P L H D A A G L V K L H V S S Y Q A V
 TCCC GTTCTGGTCTTGCAAGGTGTGGAACCTTGGCAAAGCAGGTTGCTGCAGTTGGCGAC
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 S G S G L A G V E T L A K Q V A A V G D
 CACAACGTTGAGTTCGTCCATGATGGACAGGCTGCTGACGCACGCGATGTCGGACCTTAC
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 H N V E F V H D G Q A A D A G D V G P Y
 GTTTCCTCAATCGCTTACAACGTGCTGGCATTGCGCGAAACCTCGTCGATGACGGCACC
 601 -----+-----+-----+-----+-----+-----+-----+ 660
 V S P I A Y N V L P F A G N L V D D G T
 TTCGAAACCGACGAAGAGCAGAAGCTGCGCAACGAATCCCGCAAGATTGTCGGCCTCCCA
 661 -----+-----+-----+-----+-----+-----+-----+ 720
 F E T D E E Q K L R N E S R K I L G L P
 GACCTCAAGGTCTCAGGCACCTGCGTCCGCGTGCCGGTTTTCACCGGCCACACGCTGACC
 721 -----+-----+-----+-----+-----+-----+-----+ 780
 D L K V S G T C V R V P V F T G H T L T
 ATTCACGCCGAATTCGACAAGGCAATCAGCGTCGAGCAGGCGCAGGAGATCTTGGGTGCC
 781 -----+-----+-----+-----+-----+-----+-----+ 840
 I H A E F D K A I T V E Q A Q E I L G A
 GCTTCAGGCGTCGAGCTTGTCGACGTCCCAACCCCACTTGGACCTGCCGGCATTGACGAA
 841 -----+-----+-----+-----+-----+-----+-----+ 900
 A S G V E L V D V P T P L A A A G I D E

FIG.3A

Appl. No. 10/067,974, Filed: February 8, 2002
 Dkt. No. 1533 2640001/MAC/M-G; Group Art Unit. 1645
 Inventors: Li *et al*; Tel: 202/371-2600
 Title: Polynucleotide Constructs for Increased Lysine
 Production

```

SEQ ID NO: 3      TCCCTCGTTGGACGCATCCGTCAGGACTCCACTGTCGACGACAACCGCGGTCTGGTTCTC
  (CONT.) 901      -----+-----+-----+-----+-----+-----+
SEQ ID NO: 4      S L V G R I R Q D S T V D D N R G L V L
  (CONT.)          -----+-----+-----+-----+-----+-----+
961               GTCGTATCTGGCGATAACCTTCGCAAGGGCGCAGCACTGAACACCATTCAGATTGCTGAG
                  -----+-----+-----+-----+-----+-----+
                  V V S G D N L R K G A A L N T I Q I A E
1021              CTGCTGGTTAAGTAA
                  -----+-----1035
                  L L V K *
    
```

FIG.3B

Amino Acid sequence of dapB

SEQ ID NO: 5 ATGGGAATCAAGGTTGGCGTTCTCGGAGCCAAAGGCCGTGTTGGTCAAACCTATTGTGGCA
 1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
 SEQ ID NO: 6 M G I K V G V L G A K G R V G Q T I V A
 GCAGTCAATGAGTCCGACGATCTGGAGCTTGTTCAGAGATCGGCGTCGACGATGATTTG
 61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
 A V N E S D D L E L V A E I G V D D D L
 AGCCTTCTGGTAGACAACGGCGCTGAAGTTGTCGTTGACTTCACCACTCCTAACGCTGTG
 121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
 S L L V D N G A E V V V D F T T P N A V
 ATGGGCAACCTGGAGTTCTGCATCAACAACGGCATTCTGCGGTTGTTGGAACCACGGGC
 181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
 M G N L E F C I N N G I S A V V G T T G
 TTCGATaATGCTCGTTTGGAGCAGGTTGCGGcCTGGCTTGAAGGAAAAGACAATGTCGGT
 241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
 F D N A R L E Q V R A W L E G K D N V G
 GTTCTGATCGCACCTAACTTTGCTATCTCTGCGGTGTTGACCATGGTCTTTTCCAAGCAG
 301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
 V L I A P N F A I S A V L T M V F S K Q
 GCTGCCCCGCTTCTTCGAATCAGCTGAAGTTATTGAGCTGCACCACCCCAACAAGCTGGAT
 361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
 A A R F F E S A E V I E L H H P N K L D
 GCACCTTCAGGCACCGCGATCCACACTGCTCAGGGCATTGCTGCGGCACGCAAAGAAGCA
 421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
 A P S G T A I H T A Q G I A A A R K E A
 GGCATGGACGCACAGCCAGATGCGACCGAGCAGGCACTTGAGGGTCCCGTGGCGCAAGC
 481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
 G M D A Q P D A T E Q A L E G S R G A S
 GTAGATGGAATCCCaGTTCAcGCAGTCCGCATGTCCGGCATGGTTGCTCACGAGCAAGTT
 541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
 V D G I P V H A V R M S G M V A H E Q V
 ATCTTTGGCACCCAGGGTCAGACCTTGACCATCAAGCAGGACTCCTATGATCGCAACTCA
 601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
 I F G T Q G Q T L T I K Q D S Y D R N S
 TTTGCACCAGGTGTCTTGGTGGGTGTGCGCAACATTGCACAGCACCCAGGCCTAGTCGTA
 661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
 F A P G V L V G V R N I A Q H P G L V V
 GGACTTGAGCATTACCTAGGCCTGTAA
 721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 747
 G L E H Y L G L *

FIG.4

SEQ ID NO: 10 Amino Acid sequence of ddh

SEQ ID NO: 7 1 ATGGATTTTCGGTAAGCTCGACCAGCACAGTGCCACCACAATTTTCCACCATTACAAGAAC 60
 SEQ ID NO: 8 1 M H F G K L D Q D S A T T I L E D Y K N
 61 ATGACCAACATCCGCCTAGCTATCGTAGGGTACGGAAACCTGCGACCCAGCGTCGAAAAG 120
 61 M T N I R V A I V G Y G N L G R S V E K
 121 CTTATTGCCAAGCAGCCCGACATGGACCTTGTAGGAATCTTCTCGCGCCGGGCCACCCCTC 180
 121 L I A K Q P D M D L V G I F S R R A T L
 181 GACACAAAGACGCCAGTCTTTGATGTGCGCGACGTGGACAAGCACCCCGACGACGTGGAC 240
 181 D T K T P V F D V A D V D K H A D D V D
 241 GTGCTGTTCTGTGCATGGGCTCCGCCACCGACATGCCTGAGCAGGCACCAAAGTTCGCG 300
 241 V L F L C M G S A T D I P E Q A P K F A
 301 CAGTTCGCCTGCACCGTAGACACCTACCACAACCACCGCGACATCCACGCCACCGCCAG 360
 301 Q F A C T V D T Y D N H R D I P R H R Q
 361 GTCATGAACGAAGCCGCCACCGCAGCCGGCAACGTTGCACTGGTCTGTACCGGCTGGGAT 420
 361 V M N E A A T A A G N V A L V S T G W D
 421 CCAGGAATGTTCTCCATCAACCGCTCTACGCAGCCGCACTCTTAGCCGAGCACCAGCAG 480
 421 P G M F S I N R V Y A A A V L A E H Q Q
 481 CACACCTTCTGGGGCCAGCTTTGTCACAGGGCCACTCCGATCCTTTGCGACGCATCCCT 540
 481 H T F W G P G L S Q G H S Q A L R R I P
 541 GCGTTCAAAAGGCcGTCCAGTACACCCTGCCATCCGAAGaAGCCCTGCAAAAAGGCCCGC 600
 541 G V Q K A V Q Y T L P S E E A L E K A R
 601 CGTCGGAAGCCGGCGACCTcACCGGAAAGCAAACCCACAAGCGCCAATGCTTCGTGGTT 660
 601 R G E A G D L T G K Q T H K R Q C F V V
 661 CCCGATGCGGCCGACACGAGCGCATCGAAAACGACATCCGCACCATCCCTGATTACTTC 720
 661 A D A A D H E R I E N D I R T M P D Y F
 721 GTTGGCTACGAAGTCAAGTCAACTTCATCGACGAAGCAAGCTTgGACgCCGAGCACACC 780
 721 V G Y E V E V N F I D E A T L D A E H T
 781 GGGATGCCACACGGcGGACACGTGATcACCACCGGCGACACCGGTGGCTTCAACCACACC 840
 781 G M P H G G H V I T T G D T G G F N H T
 841 GTGGAATACATCCTgAAGCTGGACCGAAACCCAGATTTACCGCTTctTCACAGATCCCT 900
 841 V E Y I L K L D R N P D F T A S S Q I A
 TTCGGcCGCCAGCTCACCCCATGAAGCAGCAGGGCCAAAGCGGtGCTTTACCGTGCTC

FIG.5A

Appl. No. 10/067,974; Filed February 8, 2002
 Dkt. No. 1533.2640001/MAC/M-G; Group Art Unit: 1645
 Inventors: Li *et al*; Tel. 202/371-2600
 Title. Polynucleotide Constructs for Increased Lysine
 Production

```

          901  .....+.....+.....+.....+.....+.....+ 960
                F  G  R  A  A  H  R  M  K  Q  Q  G  Q  S  G  A  F  T  V  L
SEQ ID NO: 7  GAAGTTGCTCCATACTTGCTCTCCCCgGAGAACTTGGAATGATCTGATCGCACGCGACGTC
  (CONT.)    961  .....+.....+.....+.....+.....+.....+ 1020
SEQ ID NO: 8  E  V  A  P  Y  L  L  S  P  E  N  L  D  D  L  I  A  R  D  V
  (CONT.)
          TAA
1021  --- 1023
    
```

FIG.5B

Appl. No. 10/067,974; Filed. February 8, 2002
Dkt. No. 1533.2640001/MAC/M-G; Group Art Unit: 1645
Inventors: Li *et al*; Tel: 202/371-2600
Title: Polynucleotide Constructs for Increased Lysin
Production

ORF2 Amino Acid sequence

```
SEQ ID NO: 9   GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC
1  -----+-----+-----+-----+-----+-----+-----+
SEQ ID NO: 10  M A E Q V K L S V E L I A C S S F T P P                               60

GCTGATGTTGAGTGGTCAACTCATGTTGAGGGCGCGGAAGCACTCGTCGAGTTTGCGGGT
61 -----+-----+-----+-----+-----+-----+-----+
A D V E W S T D V E G A E A L V E F A G                               120

CGTGCCTGCTACGAACTTTTGATAAGCCGAACCCTCGAACTGCTTCCAATGCTGCGTAT
121 -----+-----+-----+-----+-----+-----+-----+
R A C Y E T F D K P N P R T A S N A A Y                               180

CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG
181 -----+-----+-----+-----+-----+-----+-----+
L R H I M E V G H T A L L E H A N A T M                               240

TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTTC
241 -----+-----+-----+-----+-----+-----+-----+
Y I R G I S R S A T H E L V R H R H F S                               300

TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT
301 -----+-----+-----+-----+-----+-----+-----+
F S Q L S Q R F V H S G E S E V V V P T                               360

CTCATCGATGAAGATCCGCAGTTGCGTGAACTTTTCATGCACGCCATGGATGAGTCTCGG
361 -----+-----+-----+-----+-----+-----+-----+
L I D E D P Q L R E L F M H A M D E S R                               420

TTCGCTTTCAATGAGCTGCTTAATGCGCTGGAAGAAAACTTGGCGATGAACCGAATGCA
421 -----+-----+-----+-----+-----+-----+-----+
F A F N E L L N A L E E K L G D E P N A                               480

CTTTTAAGGAAAAAGCAGGCTCGTCAAGCAGCTCGCGCTGTGCTGCCCAACGCTACAGAG
481 -----+-----+-----+-----+-----+-----+-----+
L L R K K Q A R Q A A R A V L P N A T E                               540

TCCAGAATCGTGGTGTCTGGAACTTCCGACCCTGGAGGCATTTTCATTGGCATGCGAGCC
541 -----+-----+-----+-----+-----+-----+-----+
S R I V V S G N F R T W R H F I G M R A                               600

AGTGAACATGCAGACGTGAAATCCGCGAAGTAGCGGTAGGATGTTTAAGAAAGCTGCAG
601 -----+-----+-----+-----+-----+-----+-----+
S E H A D V E I R E V A V G C L R K L Q                               660

GTAGCAGCGCCAACTGTTTTCGGTGATTTTGAGATTGAACTTTGGCAGACGGATCGCAA
661 -----+-----+-----+-----+-----+-----+-----+
V A A P T V F G D F E I E T L A D G S Q                               720

ATGGCAACAAGCCCGTATGTCATGGACTTTTAA
721 -----+-----+-----+-----+-----+-----+-----+
M A T S P Y V M D F *                               753
```

FIG.6

Full length Amino Acid sequence of Lys A (pRS6)

SEQ ID NO: 11 ATGGCTACAGTTGAAAATTTCAATGAACTTCCCGCACACGTATGGCCACGCAATGCCGTG
1 -----+-----+-----+-----+-----+-----+ 60
SEQ ID NO: 12 M A T V E N F N E L P A H V W P R N A V
CGCCAAGAAGACGGCGTTGTCACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA
61 -----+-----+-----+-----+-----+-----+ 120
R Q E D G V V T V A G V P L P D L A E E
TACGGAACCCCACTGTTTCGTAGTCGACGAGGACGATTTCCGTTCCCGCTGTCGCGACATG
121 -----+-----+-----+-----+-----+-----+ 180
Y G T P L F V V D E D D F R S R C R D M
GCTACCGCATTCCGGTGGACCAGGCAATGTGCACTACGCATCTAAAGCGTTCCTGACCAAG
181 -----+-----+-----+-----+-----+-----+ 240
A T A F G G P G N V H Y A S K A F L T K
ACCATTCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCATCCATCAACGAA
241 -----+-----+-----+-----+-----+-----+ 300
T I A R W V D E E G L A L D I A S I N E
CTGGGCATTGCCCTGGCCGCTGGTTTCCCCGCCAGCCGTATCACCGCGCACGGCAACAAC
301 -----+-----+-----+-----+-----+-----+ 360
L G I A L A A G F P A S R I T A H G N N
AAAGGCGTAGAGTTCCTGCGCGCTTGGTTCAAACGGTGTGGGACACGTGGTGGCTGGAC
361 -----+-----+-----+-----+-----+-----+ 420
K G V E F L R A L V Q N G V G H V V L D
TCCGCACAGGAAGTAGAACTGTTGGATTACGTTGCCGCTGGTGAAGGCAAGATTCAGGAC
421 -----+-----+-----+-----+-----+-----+ 480
S A Q E L E L L D Y V A A G E G K I Q D
GTGTTGATCCGCGTAAAGCCAGGCATCGAAGCACACCCACGAGTTCATCGCCACTAGC
481 -----+-----+-----+-----+-----+-----+ 540
V L I R V K P G I E A H T H E F I A T S
CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCGCATTCTGAAGCAGCAAAA
541 -----+-----+-----+-----+-----+-----+ 600
H E D Q K F G F S L A S G S A F E A A K
GCCGCCAACACGCAGAAAACCTGAACCTGGTTGGCCTGCACTGCCACGTTGGTTCCAG
601 -----+-----+-----+-----+-----+-----+ 660
A A N N A E N L N L V G L H C H V G S Q

FIG.7A

Lys A (pRS6)

```

SEQ ID NO: 11  GTGTTTCGACGCCGAAGGCTTCAAGCTGGCAGCAGAACGCGTGTGGGCCTGTACTCACAG
  (CONT.) 661  -----+-----+-----+-----+-----+-----+-----+ 720
SEQ ID NO: 12  V F D A E G F K L A A E R V L G L Y S Q
  (CONT.)
271  ATCCACAGCGAACTGGGCGTTGCCCTTCCTGAACTGGATCTCGGTGGCGGATACGGCATT
  (CONT.) 721  -----+-----+-----+-----+-----+-----+-----+ 780
271  I H S E L G V A L P E L D L G G G Y G I
271  GCCTATACCGCAGCTGAAGAACCACTCAACGTCGCAGAAGTTGCCTCCGACCTGCTCACC
  (CONT.) 781  -----+-----+-----+-----+-----+-----+-----+ 840
271  A Y T A A E E P L N V A E V A S D L L T
271  GCAGTCGGA AAAATGGCAGCGGAACTAGGCATCGACGCACCAACCGTGCTTGTTGAGCCC
  (CONT.) 841  -----+-----+-----+-----+-----+-----+-----+ 900
271  A V G K M A A E L G I D A P T V L V E P
271  GGCCGCGCTATCGCAGGCCCTCCACCGTGACCATCTACGAAGTCGGCACCACCAAAGAC
  (CONT.) 901  -----+-----+-----+-----+-----+-----+-----+ 960
271  G R A I A G P S T V T I Y E V G T T K D
271  GTCCACGTAGACGACGACAAAACCCGCCGTTACATCGCCGTGGACGGAGGCATGTCCGAC
  (CONT.) 961  -----+-----+-----+-----+-----+-----+-----+ 1020
271  V H V D D D K T R R Y I A V D G G M S D
271  AACATCCGCCCAGCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC
  (CONT.) 1021  -----+-----+-----+-----+-----+-----+-----+ 1080
271  N I R P A L Y G S E Y D A R V V S R F A
271  GAAGGAGACCCAGTAAGCACCCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG
  (CONT.) 1081  -----+-----+-----+-----+-----+-----+-----+ 1140
271  E G D P V S T R I V G S H C E S G D I L
271  ATCAACGATGAAATCTACCCATCTGACATCACCAGCGGCGACTTCCTTGCACTCGCAGCC
  (CONT.) 1141  -----+-----+-----+-----+-----+-----+-----+ 1200
271  I N D E I Y P S D I T S G D F L A L A A
271  ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCTTCACACGGCCCGCCGTC
  (CONT.) 1201  -----+-----+-----+-----+-----+-----+-----+ 1260
271  T G A Y C Y A M S S R Y N A F T R P A V
271  GTGTCCGTCCGCGCTGGCAGCTCCCGCCTCATGCTGCGCCGCGAAACGCTCGACGACATC
  (CONT.) 1261  -----+-----+-----+-----+-----+-----+-----+ 1320
271  V S V R A G S S R L M L R R E T L D D I

```

FIG.7B

Appl. No. 10/067,974; Filed February 8, 2002
Dkt. No. 1533 2640001/MAC/M-G; Group Art Unit: 1645
Inventors: Li *et al.*; Tel: 202/371-2600
Title: Polynucleotide Constructs for Increased Lysin
Production

SEQ ID NO: 11 CTCTCACTAGAGGCATAA
(CONT.) 1321 -----+----- 1330
SEQ ID NO: 12 L S L E A *

FIG.7C

Truncated ORF2 Amino Acid sequence

```
SEQ ID NO: 13  GTGGCCGAACAAGTTAAATTGAGCGTGCAAGTTGATAGCGTGCAAGTTCTTTTACTCCACCC
1  -----+-----+-----+-----+-----+-----+-----+ 60
SEQ ID NO: 14  M A E Q V K L S V E L I A C S S F T P P

GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCGAGTTTGGGGGT
61  -----+-----+-----+-----+-----+-----+ 120
A D V E W S T D V E G A E A L V E F A G

CGTGCCTGCTACGAACTTTTGATAAGCCGAACCCTCGAACTGCTTCCAATGCTGCGTAT
121  -----+-----+-----+-----+-----+-----+ 180
R A C Y E T F D K P N P R T A S N A A Y

CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG
181  -----+-----+-----+-----+-----+-----+ 240
L R H I M E V G H T A L L E H A N A T M

TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTCC
241  -----+-----+-----+-----+-----+-----+ 300
Y I R G I S R S A T H E L V R H R H F S

TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT
301  -----+-----+-----+-----+-----+-----+ 360
F S Q L S Q R F V H S G E S E V V V P T

CTCAT
361  -----
L (I)
```

FIG.8

1

SEQ ID NO: 15 AACCGGTGTGGAGCCGACCATTCGCGAGGCTGCACTGCAACGAGGTCGTAGTTTTGGTACAT
GGCTTCTGGCCAGTTCATGGATTGGCTGCCGAAGAAGCTATAGGCATCGCCACCAGGGCCACC
GGAGTTACCGAAGATGGTGCCGTGCTTTTCGCCTTGGGCAGGGACCTTGACAAAGCCACGCT
GATATCGCCAAGTGAGGGATCAGAATAGTGCATGGGCACGTCGATGCTGCCACATTGAGCGGA
GGCAATATCTACCTGAGGTGGGCATTCTTCCCAGCGGATGTTTTCTTGCGCTGCTGCAGTGGG
CATTGATACCAAAAAGGGGCTAAGCGCAGTCGAGGCGCAAGAACTGCTACTACCTTTTTTAT
TGTCGAACGGGGCATTACGGCTCCAAGGACGTTTGTTTTCTGGGTGAGTTACCCCAAAAAGCA
TATACAGAGACCAATGATTTTTTATTAAAAAGGCAGGGATTGTTATAAGTATGGGTCGTATT
CTGTGCGACGGGTGTACCTCGGCTAGAATTTCTCCCCATGACACCAG

FIG. 9

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 Dkt No 1533.2640001/MAC/M-G; Group Art Unit: 1645
 Inventors: Li *et al.*, Tel: 202/371-2600
 Title: Polynucleotide Constructs for Increased Lysin
 Production

ATCC 13032	1		50
N13		V	
ATCC 21529		C	
Consensus		C	
		MALVVQKYGG SSLESAERIR NVAERIVATK KAGNDVVVVC SAMGDTTDEL	
	51		100
ATCC 13032			
N13			
ATCC 21529			
Consensus		LELAAAVNPV PPAREMDMLL TAGERISNAL VAMAIESLGA EAQSF TGSQA	
	101		150
ATCC 13032			
N13			
ATCC 21529			
Consensus		GVL TTERHGN ARIVDVTPGR VREALDEGKI CIVAGFQGVN KETRDVTTLG	
	151		200
ATCC 13032			
N13			
ATCC 21529			
Consensus		RGGS DTTAVA LAAALNADVC EIYSDVDGVY TADPRIVPNA QKLEKLSFEE	
	201		250
ATCC 13032			
N13			
ATCC 21529			
Consensus		MLELAAVGSK ILVLR SVEYA RAFNVPLRVR SSYSNDPGTL IAGSMEDIPV	
	251		300
ATCC 13032			
N13			
ATCC 21529			
Consensus		EEAVLTGVAT DKSEAKVTVL GISDKPGEAA KVFRALADAE INIDMVLQNV	
	301		350
ATCC 13032		S	G
N13		A	D
ATCC 21529		A	G
Consensus		SSVEDGTTDI TFTCPRADGR RAMEILKKLQ VQGNWTNLVY DDQVGK VSLV	
	351		400
ATCC 13032		T	
N13		T	
ATCC 21529		I	
Consensus		GAGMKSHPGV TAEFMEALRD VNVNIELIST SEIRISVLIR EDDL DAAAARA	
	401	421	
ATCC 13032			
N13			
ATCC 21529			
Consensus		LHEQFQLGGE DEAVVYAGTG R	

FIG.10

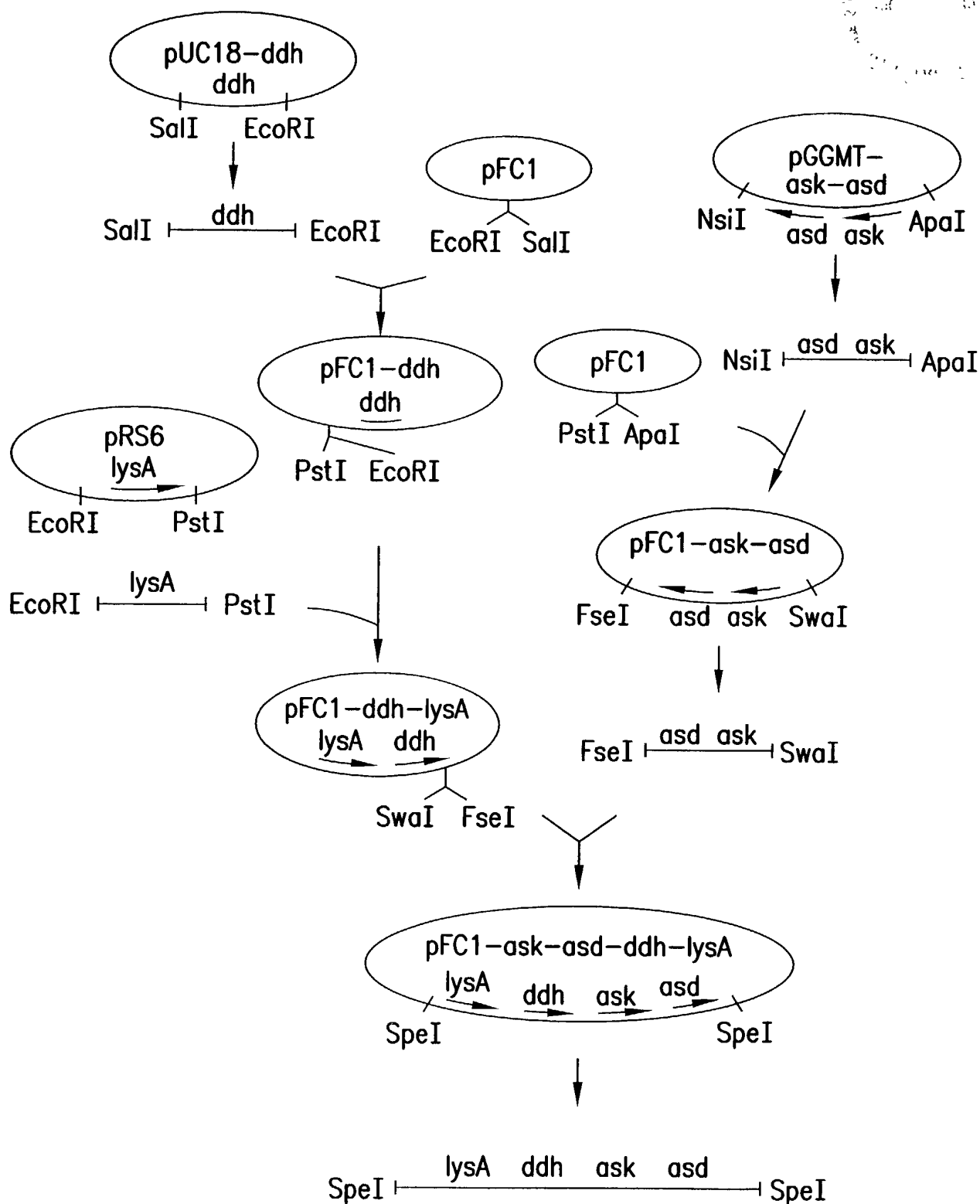


FIG. 11A

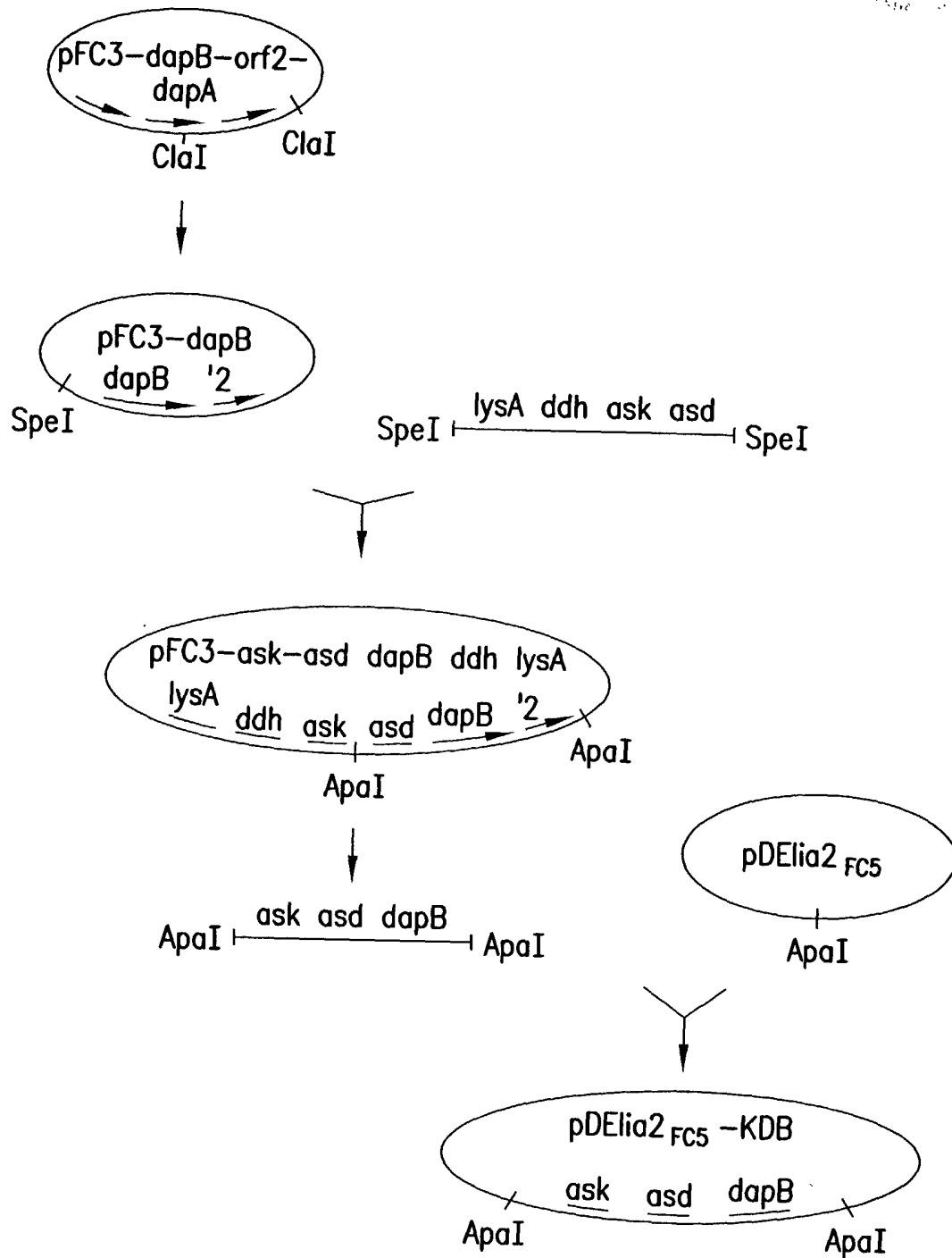


FIG. 11B

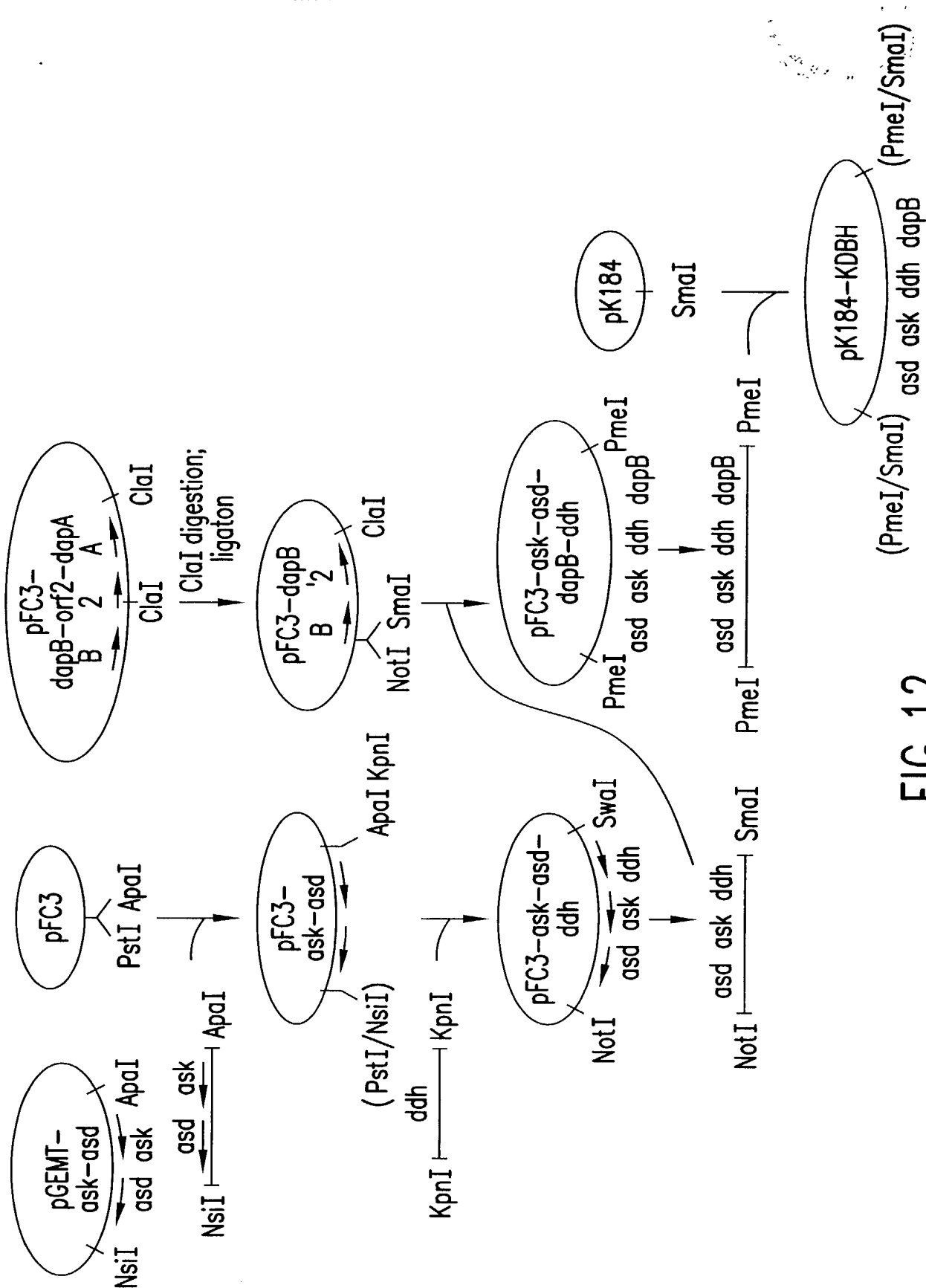


FIG. 12

pDElia2_{FC5} -ask-asd-dapB-orf2

(pDElia2_{FC5} -KDB2)

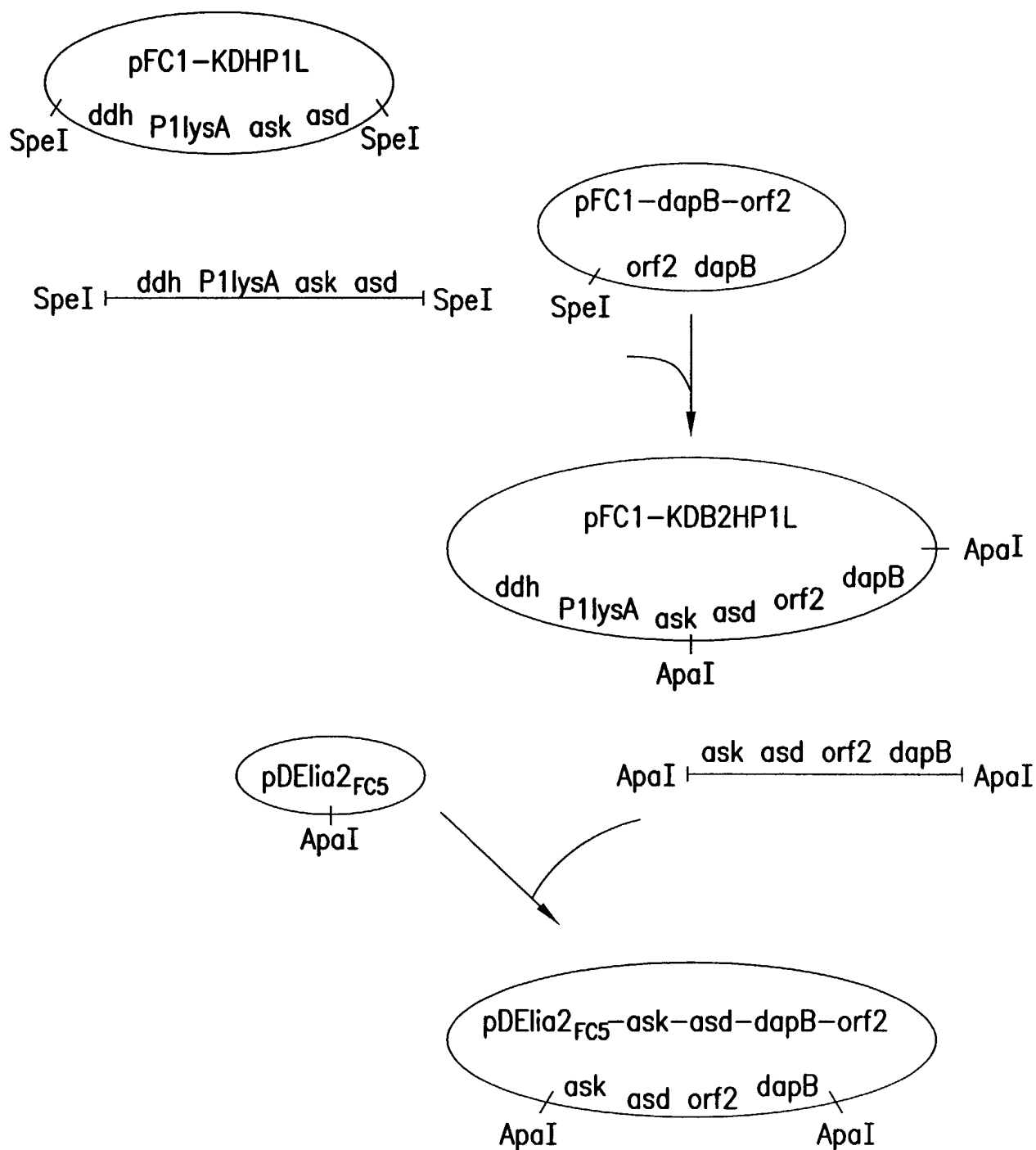


FIG. 13

pDElia2_{FC5}-ask-asd-dapB-orf2-ddh-P1lysA

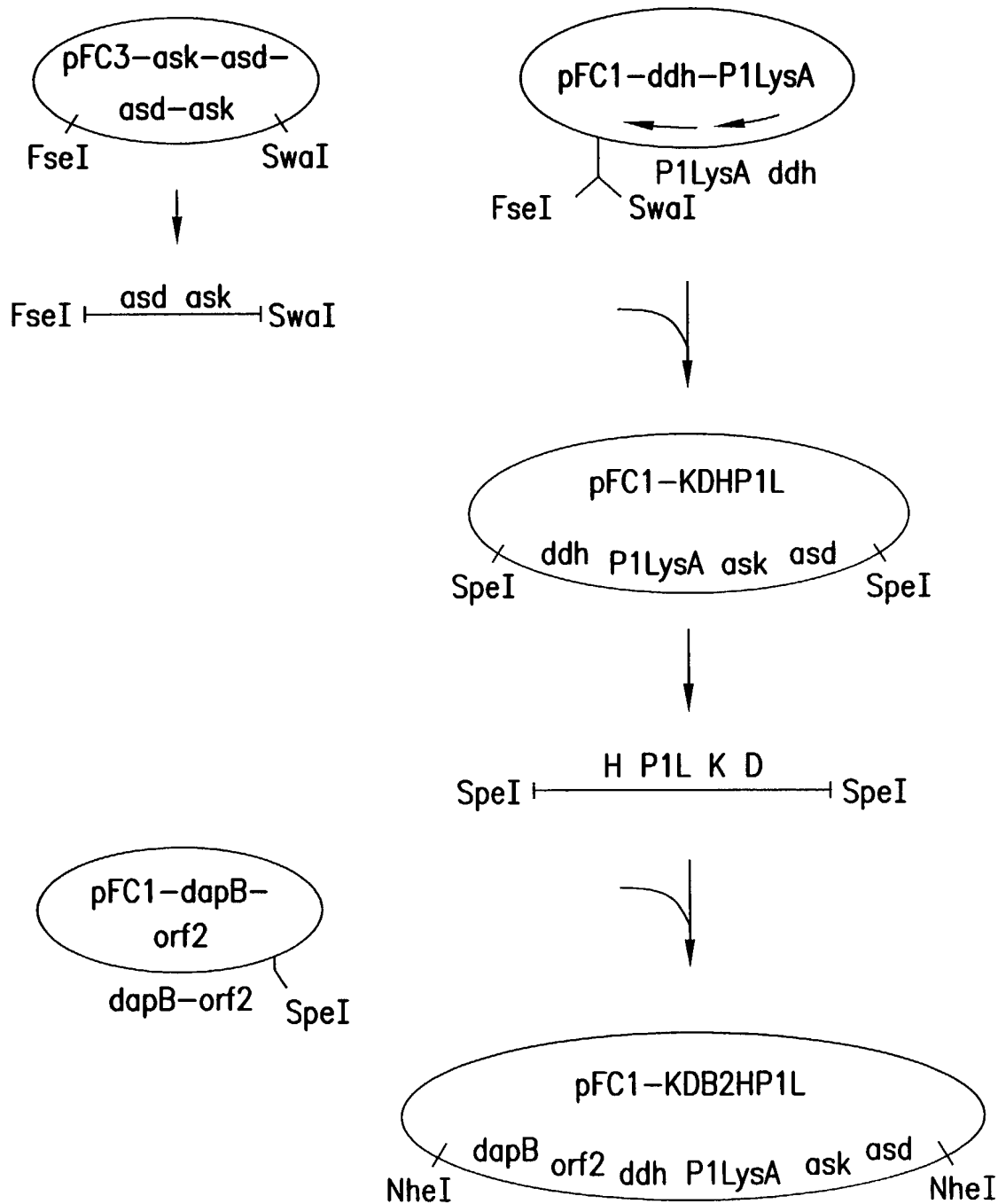


FIG. 14A

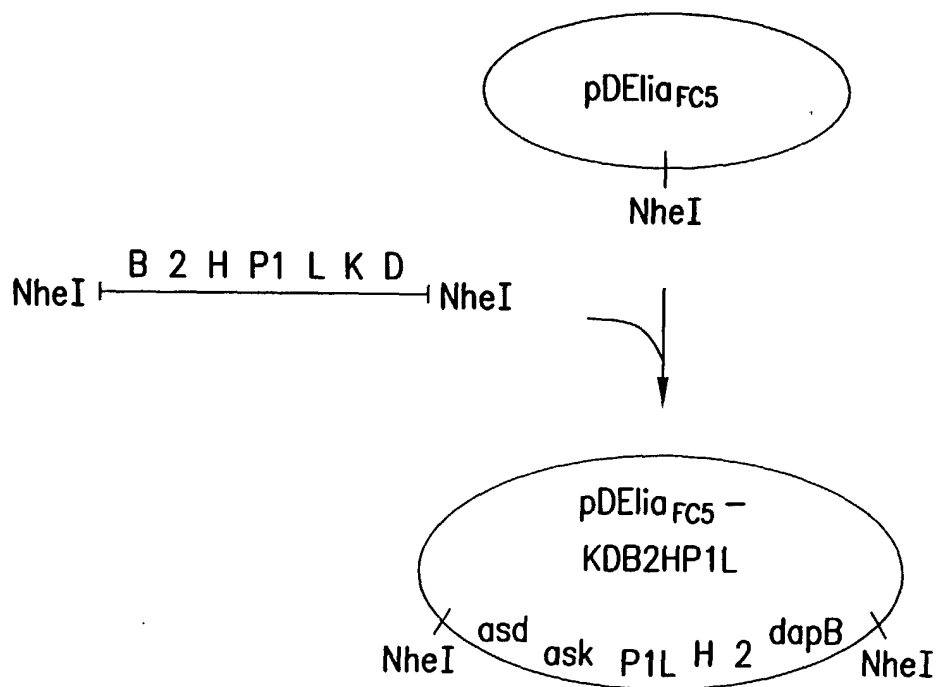


FIG. 14B